

```

AAGTAAAAGAAAGAGCGAGAAATCATCGAAATGGATTTTCATCTCATCTCTTATCGTTGGC
1 -----+-----+-----+-----+-----+ 60
TTCATTTTCTTTCTCGCTCTTTAGTAGCTTTACCTAAAGTAGAGTAGAGAATAGCAACCG

a K * K K E R E I I E (M) D F I S S L I V G -
b S K R K S E K S S K W I S S H L L S L A -
c V K E R A R N H R N G F H L I S Y R W L -

TGTGCTCAGGTGTTGTGTGAATCTATGAATATGGCGGAGAGAAGAGGACATAAGACTGAT
61 -----+-----+-----+-----+-----+ 120
ACACGAGTCCACAACACACTTAGATACTTATACGCCTCTCTTCTCCTGTATTCTGACTA

a C A Q V L C E S M N M A E R R G H K T D -
b V L R C C V N L * I W R R E E D I R L I -
c C S G V V * I Y E Y G G E K R T * D * S -

CTTAGACAAGCCATCACTGATCTTGAAACAGCCATCGGTGACTTGAAGGCCATACGTGAT
121 -----+-----+-----+-----+-----+ 180
GAATCTGTTCCGTAGTGACTAGAACTTTGTGCGGTAGCCACTGAACTTCCGGTATGCACTA

a L R Q A I T D L E T A I G D L K A I R D -
b L D K P S L I L K Q P S V T * R P Y V M -
c * T S H H * S * N S H R * L E G H T * * -

GACCTGACTTTACGGATCCAACAAGACGGTCTAGAGGGACGAAGCTGCTCAAATCGTGCC
181 -----+-----+-----+-----+-----+ 240
CTGGACTGAAATGCCTAGGTTGTTCTGCCAGATCTCCCTGCTTCGACGAGTTTAGCACGG

a D L T L R I Q Q D G L E G R S C S N R A -
b T * L Y G S N K T V * R D E A A Q I V P -
c P D F T D P T R R S R G T K L L K S C Q -

AGAGAGTGGCTTAGTGCGGTGCAAGTAACGGAGACTAAAACAGCCCTACTTTTAGTGAGG
241 -----+-----+-----+-----+-----+ 300
TCTCTACCGAATCAGCCACGTTTATTGCCTCTGATTTTGTGCGGATGAAATCACTCC

a R E W L S A V Q V T E T K T A L L L V R -
b E S G L V R C K * R R L K Q P Y F * * G -
c R V A * C G A S N G D * N S P T F S E V -

TTTAGGCGTCGGGAACAGAGGACGCGAATGAGGAGGAGATACCTCAGTTGTTTCGGTTGT
301 -----+-----+-----+-----+-----+ 360
AAATCCGCAGCCCTTGTCTCTGCGCTTACTCCTCCTCTATGGAGTCAACAAAGCCAACA

a F R R R E Q R T R M R R R Y L S C F G C -
b L G V G N R G R E * G G D T S V V S V V -
c * A S G T E D A N E E E I P Q L F R L C -

GCCGACTACAACTGTGCAAGAAGGTTTCTGCCATATTGAAGAGCATTGGTGAGCTGAGA
361 -----+-----+-----+-----+-----+ 420
CGGCTGATGTTTGACACGTTCTTCCAAAGACGGTATAACTTCTCGTAACCACTCGACTCT

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Fig. 2A

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a  A D Y K L C K K V S A I L K S I G E L R -
b  P T T N C A R R F L P Y * R A L V S * E -
c  R L Q T V Q E G F C H I E E H W * A E R -

GAACGCTCTGAAGCTATCAAAACAGATGGCGGGTCAATTCAAGTAACTTGTAGAGAGATA
421 -----+-----+-----+-----+-----+ 480
CTTGCGAGACTTCGATAGTTTGTCTACCGCCAGTTAAGTTCATTGAACATCTCTCTAT

a  E R S E A I K T D G G S I Q V T C R E I -
b  N A L K L S K Q M A G Q F K * L V E R Y -
c  T L * S Y Q N R W R V N S S N L * R D T -

CCCATCAAGTCCGTTGTCTCGGAAATACCACGATGATGGAACAGGTTTTGGAATTTCTCAGT
481 -----+-----+-----+-----+-----+ 540
GGGTAGTTCAGGCAACAGCCTTTATGGTGCTACTACCTTGTCCTCCAAACCTTAAAGAGTCA

a  P I K S V V G N T T M M E Q V L E F L S -
b  P S S P L S E I P R * W N R F W N F S V -
c  H Q V R C R K Y H D D G T G F G I S Q * -

GAAGAAGAAGAAAGAGGAATCATTGGTGTTTATGGACCTGGTGGGGTTGGGAAGACAACG
541 -----+-----+-----+-----+-----+ 600
CTTCTTCTTCTTTCTCCTTAGTAACCACAAATACCTGGACCACCCCAACCCTTCTGTTGC

a  E E E E R G I I G V Y G P G G V G K T T -
b  K K K K E E S L V F M D L V G L G R Q R -
c  R R R K R N H W C L W T W W G W E D N V -

TTAATGCAGAGCATTAAACAACGAGCTGATCACAAAAGGACATCAGTATGATGTACTGATT
601 -----+-----+-----+-----+-----+ 660
AATTACGTCTCGTAATTGTTGCTCGACTAGTGTTCCTGTAGTCATACTACATGACTAA

a  L M Q S I N N E L I T K G H Q Y D V L I -
b  * C R A L T T S * S Q K D I S M M Y * F -
c  N A E H * Q R A D H K R T S V * C T D L -

TGGGTTCAAATGTCCAGAGAATTCTGCGGAGTGTTACAATTCAGCAAGCCGTTGGAGCACGG
661 -----+-----+-----+-----+-----+ 720
ACCCAAGTTTACAGGTCTCTTAAGCCGCTCACATGTTAAGTCGTTCCGCAACCTCGTGCC

a  W V Q M S R E F G E C T I Q Q A V G A R -
b  G F K C P E N S A S V Q F S K P L E H G -
c  G S N V Q R I R R V Y N S A S R W S T V -

TTGGGTTTATCTTGGGACGAGAAGGAGACCGGCGAAAACAGAGCTTTGAAGATATACAGA
721 -----+-----+-----+-----+-----+ 780
AACCCAAATAGAACCCTGCTCTTCTCTGCGCGCTTTTGTCTCGAACTTCTATATGTCT

a  L G L S W D E K E T G E N R A L K I Y R -
b  W V Y L G T R R R P A K T E L * R Y T E -
c  G F I L G R E G D R R K Q S F E D I Q S -

GCTTTGAGACAGAAACGTTTCTTGTGTTGCTAGATGATGTCTGGGAAGAGATAGACTTG
781 -----+-----+-----+-----+-----+ 840
CGAAACTCTGTCTTTGCAAAGAACAACAACGATCTACTACAGACCCTTCTCTATCTGAAC

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Fig. 2B

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a   A L R Q K R F L L L L D D V W E E I D L -
b   L * D R N V S C C C * M M S G K R * T W -
c   F E T E T F L V V A R * C L G R D R L G -

GAGAAACTGGAGTTCCTCGACCTGACAGGGAAAACAAATGCAAGGTGATGTTACAGACA
841 -----+-----+-----+-----+-----+ 900
CTCTTTTGACCTCAAGGAGCTGGACTGTCCCTTTTGTTCGTTCCACTACAAGTGCTGT

a   E K T G V P R P D R E N K C K V M F T T -
b   R K L E F L D L T G K T N A R * C S R H -
c   E N W S S S T * Q G K Q M Q G D V H D T -

CGGTCTATAGCATTATGCAACAATATGGGTGCGGAATACAAGTTGAGAGTGGAGTTTCTG
901 -----+-----+-----+-----+-----+ 960
GCCAGATATCGTAATACGTTGTTATACCCACGCCTTATGTTCAACTCTCACCTCAAAGAC

a   R S I A L C N N M G A E Y K L R V E F L -
b   G L * H Y A T I W V R N T S * E W S F W -
c   V Y S I M Q Q Y G C G I Q V E S G V S G -

GAGAAGAAACACGCGTGGGAGCTGTTCTGTAGTAAGGTATGGAGAAAAGATCTTTTAGAG
961 -----+-----+-----+-----+-----+ 1020
CTCTTCTTTGTGCGCACCCCTCGACAAGACATCATTCCATACCTCTTTTCTAGAAAATCTC

a   E K K H A W E L F C S K V W R K D L L E -
b   R R N T R G S C S V V R Y G E K I F * S -
c   E E T R V G A V L * * G M E K R S F R V -

TCATCATCAATTGCGCCGGCTCGCGGAGATTATAGTGAGTAAATGTGGAGGATTGCCACTA
1021 -----+-----+-----+-----+-----+ 1080
AGTAGTAGTTAAGCGGCCGAGCGCCTCTAATATCACTCATTTACACCTCCTAACGGTGAT

a   S S S I R R L A E I I V S K C G G L P L -
b   H H Q F A G S R R L * * V N V E D C H * -
c   I I N S P A R G D Y S E * M W R I A T S -

GCGTTGATCACTTTAGGAGGAGCCATGGCTCATAGAGAGACAGAAGAAGAGTGATCCAT
1081 -----+-----+-----+-----+-----+ 1140
CGCAACTAGTGAAATCCTCCTCGGTACCGAGTATCTCTGTCTTCTTCTCACCTAGGTA

a   A L I T L G G A M A H R E T E E E W I H -
b   R * S L * E E P W L I E R Q K K S G S M -
c   V D H F R R S H G S * R D R R R V D P C -

GCTAGTGAAGTTCTGACTAGATTTCCAGCAGAGATGAAGGGTATGAACATGTATTTGCC
1141 -----+-----+-----+-----+-----+ 1200
CGATCACTTCAAGACTGATCTAAAGSTCGTCTCTACTTCCCATACTTGATACATAAACGG

a   A S E V L T R F P A E M K G M N Y V F A -
b   L V K F * L D F Q Q R * R V * T M Y L P -
c   * * S S D * I S S R D E G Y E L C I C P -

CTTTTGAAATTCAGCTACGACAACCTCGAGAGTGATCTGCTTCGGTCTTGTTCCTTGAC
1201 -----+-----+-----+-----+-----+ 1260
GAAAACTTTAAGTCGATGCTGTTGGAGCTCTCACTAGACGAAGCCAGAACAAGAACATG

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Fig. 2C

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a   L L K F S Y D N L E S D L L R S C F L Y -
b   F * N S A T T T S R V I C F G L V S C T -
c   F E I Q L R Q P R E * S A S V L F L V L -

      TGC GCTT TATT CCCAGAAGAACATTCTATAGAGATCGAGCAGCTTGTTGAGTACTGGGTC
1261 -----+-----+-----+-----+-----+-----+-----+ 1320
      ACGCGAAATAAGGGTCTTCTTGTAAAGATATCTCTAGCTCGTCAACAACATCATGACCCAG

a   C A L F P E E H S I E I E Q L V E Y W V -
b   A L Y S Q K N I L * R S S S L L S T G S -
c   R F I P R R T F Y R D R A A C * V L G R -

      GCGGAAGGGTTTCTCACCAGCTCCCATGGCGTTAACACCATTACAGGGATATTTTCTC
1321 -----+-----+-----+-----+-----+-----+-----+ 1380
      CCGCTTCCCAAAGAGTGGTCGAGGGTACCGCAATTGTGGTAAATGTTCCCTATAAAAGAG

a   G E G F L T S S H G V N T I Y K G Y F L -
b   A K G F S P A P M A L T P F T R D I F S -
c   R R V S H Q L P W R * H H L Q G I F S H -

      ATTGGGGATCTGAAAGCGGCATGTTTGTGGAAACCGGAGATGAGAAAACACAGGTGAAG
1381 -----+-----+-----+-----+-----+-----+-----+ 1440
      TAACCCCTAGACTTTTCGCCGTACAAACAACCTTTGGCCTCTACTCTTTTGTGTCCACTTC

a   I G D L K A A C L L E T G D E K T Q V K -
b   L G I * K R H V C W K P E M R K H R * R -
c   W G S E S G M F V G N R R * E N T G E D -

      ATGCATAATGTGGTCAGAAGCTTTGCATTGTGGATGGCATCTGAACAGGGGACTTATAAG
1441 -----+-----+-----+-----+-----+-----+-----+ 1500
      TACGTATTACACCAGTCTTCGAAACGTAACACCTACCGTAGACTTGTCCCCTGAATATTC

a   M H N V V R S F A L W M A S E Q G T Y K -
b   C I M W S E A L H C G W H L N R G L I R -
c   A * C G Q K L C I V D G I * T G D L * G -

      GAGCTGATCCTAGTTGAGCCTAGCATGGGACATACTGAAGCTCCTAAAGCAGAAAACCTGG
1501 -----+-----+-----+-----+-----+-----+-----+ 1560
      CTCGACTAGGATCAACTCGGATCGTACCCTGTATGACTTCGAGGATTTTCGTCTTTTGACC

a   E L I L V E P S M G H T E A P K A E N W -
b   S * S * L S L A W D I L K L L K Q K T G -
c   A D P S * A * H G T Y * S S * S R K L A -

      CGACAAGCGTTGGTGATCTCATTGTTAGATAACAGAATCCAGACCTTGCCTGAAAAACTC
1561 -----+-----+-----+-----+-----+-----+-----+ 1620
      GCTGTTGCAACCACTAGAGTAACAATCTATTGTCTTAGGTCTGGAACGGACTTTTTGAG

a   R Q A L V I S L L D N R I Q T L P E K L -
b   D K R W * S H C * I T E S R P C L K N S -
c   T S V G D L I V R * Q N P D L A * K T H -

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Fig. 2D

ATATGCCCGAACTGACAACACTGATGCTCCAACAGAACAGCTCTTTGAAGAAGATTCCA
 1621 -----+-----+-----+-----+-----+-----+ 1680
 TATACGGGCTTTGACTGTTGTGACTACGAGTTGTCTTGTGCGAGAACTTCTTCTAAGGT

 a I C P K L T T L M L Q Q N S S L K K I P -
 b Y A R N * Q H * C S N R T A L * R R F Q -
 c M P E T D N T D A P T E Q L F E E D S N -

 ACAGGGTTTTTCATGCATATGCCTGTTCTCAGAGTCTTGGACTTGTGCTTCACAAGTATC
 1681 -----+-----+-----+-----+-----+-----+ 1740
 TGTCCTCAAAAAGTACGTATACGGACAAGAGTCTCAGAACCTGAACAGCAAGTGTTCATAG

 a T G F F M H M P V L R V L D L S F T S I -
 b Q G F S C I C L F S E S W T C R S Q V S -
 c R V F H A Y A C S Q S L G L V V H K Y H -

 ACTGAGATTCCGTTGTCTATCAAGTATTTGGTGGAGTTGTATCATCTGTCTATGTCAGGA
 1741 -----+-----+-----+-----+-----+-----+ 1800
 TGACTCTAAGGCAACAGATAGTTCATAAACCACCTCAACATAGTAGACAGATACAGTCCT

 a T E I P L S I K Y L V E L Y H L S M S G -
 b L R F R C L S S I W W S C I I C L C Q E -
 c * D S V V Y Q V F G G V V S S V Y V R N -

 ACAAAGATAAGTGTATTGCCACAGGAGCTTGGGAATCTTAGAAAAGTGAAGCATCTGGAC
 1801 -----+-----+-----+-----+-----+-----+ 1860
 TGTTTCTATTACATAACGGTGTCTCGAACCCCTTAGAATCTTTTGACTTCGTAGACCTG

 a T K I S V L P Q E L G N L R K L K H L D -
 b Q R * V Y C H R S L G I L E N * S I W T -
 c K D K C I A T G A W E S * K T E A S G P -

 CTACAAAGAACTCAGTTTCTTCAGACGATCCCACGAGATGCCATATGTTGGCTGAGCAAG
 1861 -----+-----+-----+-----+-----+-----+ 1920
 GATGTTTCTTGAGTCAAAGAAGTCTGCTAGGGTGCTCTACGGTATACAACCGACTCGTTC

 a L Q R T Q F L Q T I P R D A I C W L S K -
 b Y K E L S F F R R S H E M P Y V G * A S -
 c T K N S V S S D D P T R C H M L A E Q A -

 CTCGAGGTTCTGAACTTGTACTACAGTTACGCCGGTTGGGAAGTGCAGAGCTTTGGAGAA
 1921 -----+-----+-----+-----+-----+-----+ 1980
 GAGCTCCAAGACTTGAACATGATGTCAATGCGGCCAACCCCTTGACGTCTCGAAACCTCTT

 a L E V L N L Y Y S Y A G W E L Q S F G E -
 b S R F * T C T T V T P V G N C R A L E K -
 c R G S E L V L Q L R R L G T A E L W R R -

 GATGAAGCAGAAGAACTCGGATTCGCTGACTTGAATACTTGGAAAACCTAACCACACTC
 1981 -----+-----+-----+-----+-----+-----+ 2040
 CTACTTCGTCTTCTTGAGCCTAAGCGACTGAACCTTATGAACCTTTTGGATTGGTGTGAG

Fig. 2E

a D E A E E L G F A D L E Y L E N L T T L -
b M K Q K N S D S L T W N T W K T * P H S -
c * S R R T R I R * L G I L G K P N H T R -

GGTATCACTGTTCTCTCATTGGAGACCCTAAAACTCTCTTCGAGTTCGGTGCTTTGCAT
2041 -----+-----+-----+-----+-----+-----+ 2100
CCATAGTGACAAGAGAGTAACCTCTGGGATTTTTGAGAGAAGCTCAAGCCACGAAACGTA

a G I T V L S L E T L K T L F E F G A L H -
b V S L F S H W R P * K L S S S S S V L C I -
c Y H C S L I G D P K N S L R V R C F A * -

AAACATATACAGCATCTCCACGTTGAAGAGTGCAATGAACTCCTCTACTTCAATCTCCCA
2101 -----+-----+-----+-----+-----+ 2160
TTTGTATATGTCGTAGAGGTGCAACTTCTCACGTTACTTGAGGAGATGAAGTTAGAGGGT

a K H I Q H L H V E E C N E L L Y F N L P -
b N I Y S I S T L K S A M N S S T S I S H -
c T Y T A S P R * R V Q * T P L L Q S P I -

TCACTCACTAACCATGGCAGGAACCTGAGAAGACTTAGCATTAAAAGTTGCCATGACTTG
2161 -----+-----+-----+-----+-----+ 2220
AGTGAGTGATTGGTACCGTCCTTGGACTCTTCTGAATCGTAATTTTCAACGGTACTGAAC

a S L T N H G R N L R R L S I K S C H D L -
b H S L T M A G T * E D L A L K V A M T W -
c T H * P W Q E P E K T * H * K L P * L G -

GAGTACCTGGTCACACCCGCAGATTTTGAAAATGATTGGCTTCCGAGTCTAGAGGTTCTG
2221 -----+-----+-----+-----+-----+ 2280
CTCATGGACCAGTGTTGGGCGTCTAAAACCTTTTACTAACCGAAGGCTCAGATCTCCAAGAC

a E Y L V T P A D F E N D W L P S L E V L -
b S T W S H P Q I L K M I G F R V * R F * -
c V P G H T R R F * K * L A S E S R G S D -

ACGTTACACAGCCTTCACAACCTTAACCAGAGTGTTGGGGAAATTCTGTAAGCCAAGATTGT
2281 -----+-----+-----+-----+-----+ 2340
TGCAATGTGTCGGAAGTGTTGAATTGGTCTCACACCCCTTTAAGACATTTCGGTTCTAACA

a T L H S L H N L T R V W G N S V S Q D C -
b R Y T A F T T * P E C G E I L * A K I V -
c V T Q P S Q L N Q S V G K F C K P R L S -

CTGCGGAATATCCGTTGCATAAACATTTACACTGCAACAAGCTGAAGAATGTCTCATGG
2341 -----+-----+-----+-----+-----+ 2400
GACGCCTTATAGGCAACGTATTTGTAAAGTGACGTTGTTTCGACTTCTTACAGAGTACC

a L R N I R C I N I S H C N K L K N V S W -
b C G I S V A * T F H T A T S * R M S H G -
c A E Y P L H K H F T L Q Q A E E C L M G -

GTTTCAGAACTCCCAAAGCTAGAGGTGATTGAACTGTTTCGACTGCAGAGAGATAGAGGAA
2401 -----+-----+-----+-----+-----+ 2460
CAAGTCTTTGAGGGTTTCGATCTCCACTAACTTGACAAGCTGACGTCTCTCTATCTCCTT

Fig. 2F

a V Q K L P K L E V I E L F D C R E I E E -
b F R N S Q S * R * L N C S T A E R * R N -
c S E T P K A R G D * T V R L Q R D R G I -

TTGATAAGCGAACACGAGAGTCCATCCGTCGAAGATCCAACATTGTTCCCAAGCCTGAAG
2461 -----+-----+-----+-----+-----+ 2520
AACTATTCGCTTGTGCTCTCAGGTAGGCAGCTTCTAGGTTGTAACAAGGGTTCGGACTTC

a L I S E H E S P S V E D P T L F P S L K -
b * * A N T R V H P S K I Q H C S Q A * R -
c D K R T R E S I R R R S N I V P K P E D -

ACCTTGAGAACTAGGGATCTGCCAGAACTAAACAGCATCCTCCCATCTCGATTTCATTTC
2521 -----+-----+-----+-----+-----+ 2580
TGGAACCTCTTGATCCCTAGACGGTCTTGATTTGTCGTAGGAGGGTAGAGCTAAAAGTAAG

a T L R T R D L P E L N S I L P S R F S F -
b P * E L G I C Q N * T A S S H L D F H S -
c L E N * G S A R T K Q H P P I S I F I P -

CAAAAAGTTGAAACATTAGTCATCACAATTTGCCCCAGAGTTAAGAACTGCCGTTTCAG
2581 -----+-----+-----+-----+-----+ 2640
GTTTTTCAACTTTGTAATCAGTAGTGTTTAAACGGGGTCTCAATTCTTTGACGGCAAAGTC

a Q K V E T L V I T N C P R V K K L P F Q -
b K K L K H * S S Q I A P E L R N C R F R -
c K S * N I S H H K L P Q S * E T A V S G -

GAGAGGAGGACCCAGATGAACTTGCCAACAGTTTATTGTGAGGAGAAATGGTGGAAGCA
2641 -----+-----+-----+-----+-----+ 2700
CTCTCCTCCTGGGTCTACTTGAACGGTTGTCAAATAACACTCCTCTTTACCACCTTTTCGT

a E R R T Q M N L P T V Y C E E K W W K A -
b R G G P R * T C Q Q F I V R R N G G K H -
c E E D P D E L A N S L L * G E M V E S T -

CTGGAAAAAGATCAACCAACGAAGAGCTTTGTTATTTACCGCGCTTTGTTCCAAATTGA
2701 -----+-----+-----+-----+-----+ 2760
GACCTTTTTCTAGTTGGTTTGCTTCTCGAAACAATAAATGGCGCGAAACAAGGTTTAACT

a L E K D Q P N E E L C Y L P R F V P N * -
b W K K I N Q T K S F V I Y R A L F Q I D -
c G K R S T K R R A L L F T A L C S K L I -

TATAAGAGCTAAGAGCACTCTGTACAAATATGTCCATTCTATAAGATGCAGGAAGCCAGGA
2761 -----+-----+-----+-----+-----+ 2820
ATATTCTCGATTCTCGTGAGACATGTTTATACAGGTAAGTATTCTACGTCCTTCGGTCCT

a Y K S * E H S V Q I C P F I R C R K P G -
b I R A K S T L Y K Y V H S * D A G S Q E -
c * E L R A L C T N M S I H K M Q E A R K -

AGGTTGTTCCAGTGAAGTCATCAACTTTCCACATAGCCACAAAAGTAGAGATTATGTAAT
2821 -----+-----+-----+-----+-----+ 2880
TCCAACAAGGTCACCTTCAGTAGTTGAAAGGTGTATCGGTGTTTGTATCTCTAATACATTA

Fig. 2G

a R L F Q * S H Q L S T * P Q N * R L C N -
 b G C S S E V I N F P H S H K T R D Y V I -
 c V V P V K S S T F H I A T K L E I M * S -

CATAAAAACCAAACTATCCGCGA
 2881 -----+-----+----- 2903
 GTATTTTTGGTTTGATAGGCGCT

a H K N Q T I R -
 b I K T K L S A -
 c * K P N Y P R -

ENZYMES THAT DO CUT:

NONE

ENZYMES THAT DO NOT CUT:

KpnI

Fig. 2H

-146
ATCGATTGATCTCTGGCTCAGTGCAGTAGTCCATTTGAGAGCAGTCGTAGCCCCGCGTG -86

GCGCATCATGGAGCTATTTGGAATTTTCGAGGGTTATCGATTTCGTAGTGGGAACCCATT -26

CATTGTTTGAACCACCAACGGACGACTTAACAAGCTCCCCGAGGTGCATGATGAAAATT 35
MetLysIle

GCTCCAGTTGCCATAAATCACAGCCCCTCAGCAGGGAGGTCCCGTCACACGCGGCACCC 95
AlaProValAlaIleAsnHisSerProLeuSerArgGluValProSerHisAlaAlaPro

ACTCAGGCAAAGCAAACCAACCTTCAATCTGAAGCTGGCGATTTAGATGCAAGAAAAAGT 155
ThrGlnAlaLysGlnThrAsnLeuGlnSerGluAlaGlyAspLeuAspAlaArgLysSer

AGCGCTTCAAGCCCGGAAACCCGCGCATTACTCGCTACTAAGACAGTACTCGGGAGACAC 215
SerAlaSerSerProGluThrArgAlaLeuLeuAlaThrLysThrValLeuGlyArgHis

AAGATAGAGGTTCCGGCCTTTGGAGGGTGGTTCAAAAAGAAATCATCTAAGCACGAGACG 275
LysIleGluValProAlaPheGlyGlyTrpPheLysLysLysSerSerLysHisGluThr

GGCGGTTCAAGTGCCAACGCAGATAGTTCGAGCGTGGCTTCCGATTCCACCGAAAAACCT 335
GlyGlySerSerAlaAsnAlaAspSerSerSerValAlaSerAspSerThrGluLysPro

TTGTTCCGTCTCACGCACGTTTCCTTACGTATCCCAAGGTAATGAGCGAATGGGATGTTGG 395
LeuPheArgLeuThrHisValProTyrValSerGlnGlyAsnGluArgMetGlyCysTrp

TATGCCTGCGCAAGAATGGTTGGCCATTCTGTGCAAGCTGGGCCTCGCCTAGGGCTGCCG 455
TyrAlaCysAlaArgMetValGlyHisSerValGluAlaGlyProArgLeuGlyLeuPro

GAGCTCTATGAGGGAAGGGAGGCGCCAGCTGGGCTACAAGATTTTTCAGATGTAGAAAGG 515
GluLeuTyrGluGlyArgGluAlaProAlaGlyLeuGlnAspPheSerAspValGluArg

TTTATTACAATGAAGGATTAACCTCGGGTAGACCTTCCAGACAATGAGAGATTTACACAC 575
PheIleHisAsnGluGlyLeuThrArgValAspLeuProAspAsnGluArgPheThrHis

Fig. 3A

GAAGAGTTGGGTGCACTGTTGTATAAGCACGGGCCGATTATATTTGGGTGGAAAAC^{TC}CG 635
GluGluLeuGlyAlaLeuLeuTyrLysHisGlyProIleIlePheGlyTrpLysThrPro

AATGACAGCTGGCACATGTCGGTCCTCACTGGTGTGATAAAGAGACGTCGTCCATTACT 695
AsnAspSerTrpHisMetSerValLeuThrGlyValAspLysGluThrSerSerIleThr

TTTCACGATCCCCGACAGGGGCCGGACCTAGCAATGCCGCTCGATTACTTTAATCAGCGA 755
PheHisAspProArgGlnGlyProAspLeuAlaMetProLeuAspTyrPheAsnGlnArg

TTGGCATGGCAGGTTCCACACGCAATGCTCTACCGCTAAGTAGCAGGGTATCTTCACGTG 815
LeuAlaTrpGlnValProHisAlaMetLeuTyrArgEnd

GCGGCATCATGACAAGCCCATGATGCCGCCAGCAGCTACCTGAATGCCGTCTGGCTTTTT 875
→ ←

GGTCCCTATTGTCGTATCCGGAAGATGACGTCAAAGAATCTCGGCAAGAGCTTCTTGCT 935

CGACTCCTCAGCTTCCGGATCGATCAGGTGCTTGCCAGAGCGCGCTTGTCATGAGCAT 995

CTGCCACAGCTGCTGGTCGATGGTGTCTCAGCTAAAGGGATTTTGACGACAACCATGCG 1055

CAACTGCCCCGTTGCGATACGCTCGATCCTGAAGCCCCGGTGTCCATGGCAGCCCCAAGAA 1115

AAAGACATAGTTCGCCGCTGTGAGGTTGTAGCCTGTGCCGGCGGCCGACCTGGTCCCGAT 1175

AAACACCCTGCAGTCCGGATCCTGCTGGAAAGCATCAATCGCCTTCTGCCGCTTCTTGGG 1235

CGAGTCACTGCCCACCAACGTACGCACCCGACGCCAAGCTTGAGGCAGTGCTCCCGCAA 1295

CGTGGCCACGGATTCTTGATACTCGCAGAAGAGGATCACCTTGTCGTGAC 1346

Fig. 3B

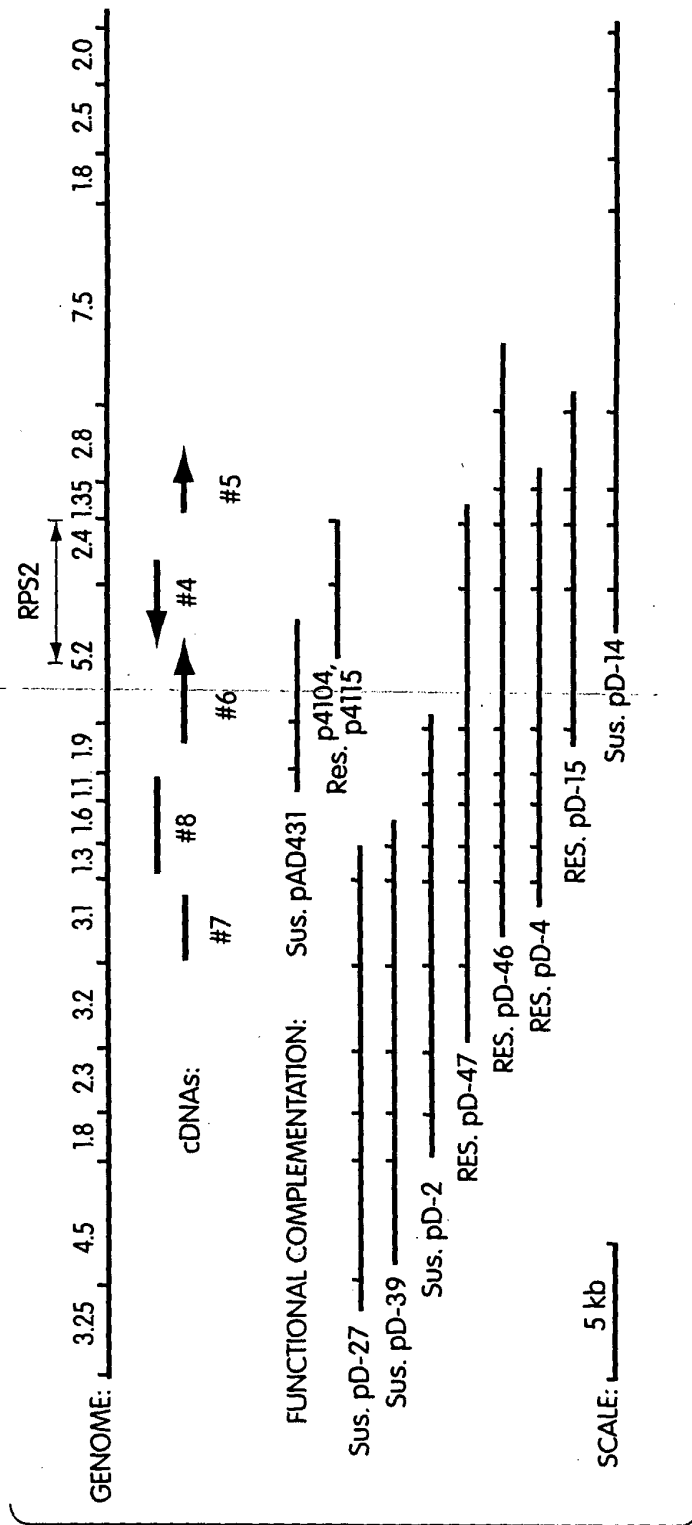


Fig. 4

	1				50
L6pro	MSYLREVATA	VALLLPFILL	NKFWRPNSKD	SIVNDDDDST	SEVDAISDST
NprotM
PrfP
rps2
	51	6			100
L6pro	NPSGSFPSVE	YEVFLSFRGP	DTREQFTDFL	YQSLRRYKIM	TFRDDDELLK
Nprot	ASSSSSRWS	YDVFLSFRGE	DTRKTFTSHL	YEVLNKGIK	TFQDDKRLEY
PrfP	LRSKLDLIID	LKHQIESVKE
rps2	MDFISSLIVG	CAQVLCESMN	MAERRGHKTD	LRQAITDLET
	101				150
L6pro	GKEIGPNLLR	AIDQSKIYVP	IISSGYADSK	WCLMELAEIV	RRQEEDPRRI
Nprot	GATIPGELCK	AIEESQFAIV	VFSENYATSR	WCLNELVKIM	ECK.TRFKQT
PrfP	GLLCLRSFID	HFSESYDEHDEA	CGLIARVSVM	AYKAE.....
rps2	AIGDLKAIRD	DLTLRIQQDG	LEGRSCSNRA	REWLSAVQVT	ETKTA.....
	151	7			200
L6pro	ILPIFYMVDP	SDVRHQTCGY	KKAFRKHANK	F..DGQTIQN	WKDALKKVG
Nprot	VIPIFYDVDP	SHVRNQKESF	AKAFEEHETK	YKDDVEGIQR	WRIALNEAAN
PrfPYVIDS	CLAYSHPLWY	KVLW.....	..IS.....	..EVLENIKLV
rps2LLLVR	FRRREQRTM	RRRY.....	..LSCFGCAD	YKLCKKVS
	201			8	250
L6pro	LKGWHIGKND	KQGAIAKVS	ADIWSHISKE	NLILE...TD	ELVIGIDHIT
Nprot	LKGSCDNRDK	TDADCIRQIV	DQISSKLCKI	SLSY....LQ	NIIVGIDTHLE
PrfP	NKVVGETCER	RNIEVTVEHV	AKTTTYVAPS	FSAYTQRANE	EMEGFQDTID
rps2	LKSIGELRER	SEAIKTDGGS	IQVTCREIPI	KSVVG.....NTTMM
	251		1	-P-loop	300
L6pro	AVLEKLSLDS	ENVTMVGLYG	MGGIGKTTTA	KAVYNKI...	..SSC.FDCC
Nprot	KIESLLEIGI	NGVRINGIWG	MGGVGKTTIA	RAIFDTLLGR	MDSSYQFDGA
PrfP	ELKDKLLGGS	PELDVISIVG	MPGLGKTTLA	KKIYNDPEVT	..SRFDVHAQ
rps2	EQVLEFLSEE	EERGIIGVYG	PGGVGKTTLM	QSINNELITK	..G....HQY
	301				350
L6pro	CFIDNIRETQ	EKDGVVVLQK	KLVSEILRID	..SGSVGFNN	DSGGRKTIKE
Nprot	CFLKDIKE..	NKRGMHSLQN	ALLSELLR..	...EKANYNN	EEDGKHQMAS
PrfP	CVVTQLYSWR	EL.LLTILND	VLEP...S..	...DRNEKED	GE.IADELRR
rps2	DVLIWVQMSR	EF.GECTIQQ	AVGA...RLG	..LSWDEKET	GENRALKIYR
	351	2		3	400
L6pro	RVSRLFILVV	LDDVDEKFKF	EDMLGSPKDF	ISQ.SRFIIT	SRSRMRVLGTL
Nprot	RLRSKKVLIV	LDDIDNKDHY	LEYLAGDLDW	FGNGSRIIIT	TRDKHLI...
PrfP	FLLTKRFLIL	IDDVWDYKVV	DNLCMCFSD.	VSNRSRIILT	TRLNDVAEYV
rps2	ALRQKRFLLL	LDDVWEEIDL	EKTGVPRPD.	RENKCKVMFT	TRSIALCENN

Fig. 5A-1

```

401                                     450
L6pro NEN.QCKLYE VGSMKPRSL ELFSKHAFKK NT....PPSY YETLANDVVD
Nprot .EK.NDIIYE VTALPDHESI QLFKQHAFGK EV....PNEN FEKLSLEVVN
PrfP .KC.ESDPHH LRLFRDDESW TLLQKEVFQG E....SCPPE LEDVGFEISK
rps2 .GA.EYK.LR VEFLEKKHAW ELFCSKVWRK DLLESSSIRR LAEI...IVS

451      4                                     500
L6pro TTAGLPLTLK VIGSLLFKQE IAV..WEDTL EQL....RRT LNLDEVYDRL
Nprot YAKGLPLALK VWGSLHNLRL LTE..WKSAL EHM....KNN .SYSGIIDNV
PrfP SCRGLPLSVV LVAGVLKQKK KTLDSWKVVE QSL..SQRI GSLEESISII
rps2 KCGGLPLALI TLGGAMAH.R ETEEEWIIHAS EVLTRFPAEM KGMNYVFALL

501      5      9                                     550
L6pro KISYDALNPE .AKEIFLDIA CFFIGQ..NK EEPYMWTD C NFYPASNIIF
Nprot KISYDGLPEK .QQEMFLDIA CFLRGE..EK DYILQILESC HIGAEYGLRI
PrfP GFSYKNL.PH YLKPCFLYFG GFLQKDIHD SKMTKLWVAE EFVQANN...
rps2 KFSYDNLES D LLRSCFLYCA LFPEEHSIEI EQLVEYWVGE GFLTSSHGVN

551      10                                     600
L6pro LIQRCMIQVG .....DD DEFKMHDQLR DMGREIVRRE DVLPWKRSRI
Nprot LIDKSLVFIS .....EY NQVQMHDLIQ DMGKYIVNFQ KD.PGERSRL
PrfP .....EY NQVQMHDLIQ DMGKYIVNFQ KD.PGERSRL
rps2 TIYKGYFLIG DLKAACLET GDEKTQVKMH NVVRSFALWM ASEQGTYKEL

601      650
L6pro WSAEEGIDLL LNKKGSSKVK AISI.PWGVK YEFK.SECFL NLSELRYLHA
Nprot WLAKEVEEVM SNNTGTNAME AIWVSSYSST LRFS.NQAVK NMKRLRVFNM
PrfP .....EY NQVQMHDLIQ DMGKYIVNFQ KD.PGERSRL
rps2 ILVEPSMGHT EAPKAENWRQ ALVISLLDNR IQTL.PEKLI CPKLTTLMLQ

651      700
L6pro REAMLTGDFN NLLPNLKWLE LPFYKHGEDD PPLTNYTMKN LII.VILEHS
Nprot GRSSTHYAID YLPNNLRCFV CTNYPW...E SFPSTFELKM LVH.LQLRH.
PrfP .....EY NQVQMHDLIQ DMGKYIVNFQ KD.PGERSRL
rps2 QNSSLKKIPT GFFMHMPVLR VLDLSF.... TSITEIPLSI KYL.VELYHL

701      750
L6pro HITADDWGGW RHMMKMAERL KVVRLASNYS LYGRRVR...
Nprot .....NSL RHLWTETKHL PSL.....RRID...
PrfP .....EY NQVQMHDLIQ DMGKYIVNFQ KD.PGERSRL
rps2 SMSGTKISVL PQELGNLRKL KHLDLQRTQF LQTIPRDAIC WLSKLEVLNL

751      800
L6pro .LSD.CWRFP KSIEVLSMTA IEMDEVDIGE LKKLKTLLVK FCPIQKISGG
Nprot .LSW.SKRLT RTPDFTGMPN LEY..VNLYQ CSNLEEVHHS LGCCSKVIGL
PrfP .....EY NQVQMHDLIQ DMGKYIVNFQ KD.PGERSRL
rps2 YYSY.AGWEL QSFGEDEAEE LGFADLEYLE NLTTLGITVL SLETCLKLFE

```

Fig. 5A-2

	801		850
L6pro	TFGMLKGLRE	L.CLEFNWGT	NLREVVADIG QLSSLKVLKT TGAKEVEINE
Nprot	YLNDCKSLKR	F.....PCVNVESLE
PrfP
rps2	FGALHKHIQH	L.HVEECNEL	LYFNLPSLTN HGRNLRRLSI KSCHDLEYLV
	851		900
L6pro	FPLGLK....	...ELSTSSR	IPNLSQLLDL EVLKVYDCKD GFDMPASPSP
Nprot	Y.LGLR....	...SCDSLEK	LPEIYGRMKP EI..... QIHMQSGSIR
PrfP
rps2	TPADFENDWL	PSLEVLTLHS	LHNLTRVWGN SVSQDCLRNI RCINISHCNK
	901		950
L6pro	EDESSVWWKV	SKLKSLEK	TRINNVVDD ASSGGHLPY LLPTSLTYLK
Nprot	ELPSSIFQYK	THVTKLL..	.WNMKNLVAL PSSICRL... ..KSLVSL
PrfP
rps2	LKNVSWVQKL	PKLEVIEFLD	CREIEELISE HESPSVEDPT LFP.SLKT
	951		1000
L6pro	IYQCTEPTWL	P.GIENLENL	TSLEVNDIFQ TLGGDLGLQ GLRSLEILRI
Nprot	VSGCSKLESL	PEEIGDLNL	RVFDASDTL.ILRP
PrfP
rps2	TRDLPELNSI	LPSRFSFQKV	ETLVITNCPR VKKLPFQERR TQMNLPVYC
	1001		1050
L6pro	RKVNGLARIK	GLKDLLCSST	CKLRKFYITE CPDLIELLPC ELGGQTVVVP
Nprot	P.....SSI	IRLNKLIILM FRGFKDGVHF EFPPVAEGLH
PrfP
rps2	EEKWWKALEK	DQPNEELCYL	PRFVPN.... ..
	1051		1100
L6pro	SMAELTIRDC	PRLEVGP MIR	SLPKFPMLKK LDLAVANITK EEDLDAIGSL
Nprot	SLEYLNL.SY	CNLIDGGLPE	EIGSLSSLKK LDLSRNNF.. EHLPPSSIAQL
PrfP
rps2
	1101		1150
L6pro	EELVSLELEL	DDTSSGIERI	VSSSKLQKLT TLVVKVPSLR EIEGLEELKS
Nprot	GALQSLDLK.DCQRLTQLP ELPPELNELH .VDCHMALKE
PrfP
rps2
	1151		1200
L6pro	LQDLYLEGCT	SLGRLPLEKL	KE.....LD IGGCPDLTEL VQTVVAVPSL
Nprot	IHDL.VTKRK	KLHRVKLDDA	HNDTMYNLFA YTMFQNISSM RHDISASDSL
PrfP
rps2

Fig. 5A-3

	1201		1250
L6pro	RGLTIRDCPR	LEVGPMIQSL	PKFPMLNELT LSMVNITKED ELEVLSLEE
Nprot	.SLTV.....	FTGQPYPEKI	PSWFHHQGWD .SSVSVNLPE NWYIPDKFLG
PrfP
rps2
	1251		1300
L6pro	LD.SLELTD	DTCSSIERIS	FLSKLQKLT LIVEVPSLRE IEGLAELKSL
Nprot	FAVCYSRSLI	DTTAHLIPVC	.DDKMSRMTQ KLALSECDTE SSNYSEWD.I
PrfP
rps2
	1301		1350
L6pro	RILYL.....EGCTSLERL WPDQQQLGSL KNLNVLDIQG
Nprot	HFFFVPFAGL	WDTSKANGKT	PNDYGIIRLS FSGECKMYGL RLLYKEGPEV
PrfP
rps2
	1351		1387
L6pro	CKSLSDHLS	ALKTTLPRA	RITWPDQPYR
Nprot	NALLQMRNS	NEPTEHSTGI	RRTQYNNRTS FYELING
PrfP
rps2

Fig. 5A-4

N 1015 SRS[.]LID[.]TTA[.]HLIPVCDDK.....MSR[.]MTQ[.]KLA....LSE[.]CD[.]TES 1049
 :..|.: .. :::|.. : :..|.:|.:|: |. | . .
 L6 1115 CPDLTEL[.]VQTVVAVPSLRGLTIRDCPRLEVGP[.]MIQSLPKFPMLNEL[.]TLSM 1164
 N 1050 SNYSEWDI[.]HFFFV[.]PFAGLWD[.]TSKANGKTPNDYGI[.]IRLSF[.]S[.]GEEKMYGL[.]RL 1099
 |... | :..:..:| . . . :.|...: |.: :| :|: .| :
 L6 1165 VNITKEDELEV[.]LGSLEEL[.]DSLELTLD[.]DTCSSIERISF.LSKLQKL[.]TTLIV 1213
 N 1100 LYKEGPEVN[.]ALLQ[.]MRENSNEPTEHSTGIRRTQYNNRTS[.]FYELIN 1143
 .. .|:::| :::. . | :|:: | : :. : .| |
 L6 1214 EVPSLREIEGLAELKSLRILYLEGCTSLER.LWPDQQQLGSLKN 1256

Fig. 5B-3

	-32	ACAAGTAAAGAGACCGAGAAATCATCGAA	-1
ATGGAATTTCATCTCATCTTATCTGCTGGCTGCTCAGGCTGTGTGTAATCTATGAATATGCGGAGAGAGAGACATTAAGACTGATCTTAGACAAGCCATCATGATCTTGAACA			120
<u>M D F I S S L I V G C A Q V L C E S M N M A E R R G H K T D L R Q A I T D L E T</u>	relatively hydrophobic		40
GCCATCGGTGACTTGAAGCCATACGTGATGATGACCTTAAAGGATCCAAAGACGGTCTAGAGGAGAGAGCTGCTCAAAATCGTCCAGAGAGTGGCTTAGTCCGGTGAAGTAACG			240
<u>A I G D L K A I R D D L T L R I Q Q D G L E G R S C S N R A R E W L S A V Q V T</u>	leucine-zipper		80
GAGACTAAACAGCCCTACTTTTACGTAGGCTTAAAGCCGTGGGAACAGAGACCGGAATGAGAGAGATACCTCAGTTGTTGGTGTGCGGACATCAAACTGTGCAAGAAAGTTTCT			360
E T K T A L L L V R F R R R E Q R T R M R R R Y L S C F G C A D Y K L C K K V S			120
GCCATATTGAGAGCATTTGGTACGTGAGAGAACGCTCTGAAGCTATCAAAACAGATGGCGGGTCATTTCAAGTAACCTGTAGAGAGATACCATCAAGTCCGTTGTGGAATPACACG			480
A I L K S I G E L R E R S E A I K T D G G S I Q V T C R E I P I K S V V G N T T			160
ATGATGGAACAGGTTTGGAAATTTCTCAGTGAAGAGAAAGAGGAATCATTTGGTATTATGACCTGGTGGGTTGGGAAGACAAAGCTTAATGCAGAGCATTAACAGAGACTGATC			600
<u>M M E Q V L E F L S E E E R G I I G V Y G P G G V G K T T L M Q S I N N E L I</u>	kinase-1a		200
ACAAAGGACATCAGTATGATGACTGATTTGGGTTCAAAATCTCCAGAGAAATTCGGCGAGTGTACAATTACAGCAAGCCGTTGGAGACAGGTTGGTTAATCTTGGAGCAGAGAGAGACC			720
<u>T K G H Q Y D V L I W V Q M S R E F G E C T I Q Q A V G A R L G L S W D E K E T</u>			240
GGGGAACACAGAGCTTTGAAGATATACAGAGCTTTGAGACAGAAACGTTTCTGTGTTGTAGATGANGTCTGGGAGAGATAGACTTTGAGAAACTGAGAGTTCTCGACCTGACAGG			840
<u>G E N R A L K I Y R A L R Q K R F L L L L D D V W E E I D L E K T G V P R P D R</u>	kinase-2		280

Fig. 6A

GAAAAAATGCCAAGTGATGTTACGACACGGCTTATGACATTATGCCAATATGCGGATATACAGTTGAGACTGGAGTTTCTGAGAGAAGAACACCGCTGGAGCTGTTCTGT
 ENKCKVMFTTFRSIALCNMMGA EYKLRVEFL EKKHAWELFC 960 320
 AGTAAGTATGGAGAAAGATCTTTTAGAGTCATCAATTCGCCGGCTCGCGAGATTATAGTGAATAATGTGAGAGATTGCCACTAGCCTTGATCATTAGAGAGACCATGGCT 1080
 SKVWRKDLLESSSIRRLAEII VSKCGGLPLALITLGGA MA 360
 kinase-3a
 membrane integrated
 CATAGAGACAGAGAAGAGTGGATCCATGCTAGTGAAGTTCTGACTAGATTCCAGCAGAGATGAAGGGTATGAACCTATGTATTTGCCCTTTTGAATTCAGCTACGACAACCTCGAG 1200
 HRETEEWIHASEVLT RFP AEMKGM NYVFALLKF SYD NLE 400
 AGTGAATCTGCTTCGGTCTTCTTCTGTACTGCGCTTTATTTCCAGAGAACAATTCTAATAGAGATCGAGCAGCTTTGTGAGTACTGGGTCGGCGAAGGGTTTCTACCAAGCTCCCATGGC 1320
 S D L L R S C F L Y C A L F P E E H S I E I E Q L V E Y W V G E G F L T S S H G 440
 GTTAACACCAATTTACAAGGATATTTCTCATTTGGGATCGAAGCGGCAATGTTGTTGGAACCGGAGATGAGAAAACACAGGTGAAGATGCATTAATGTGTCAGAGCTTTGCATTG 1440
 V N T I Y K G Y F L I G D L K A A C L L E T G D E K T Q V K M H N V V R S F A L 480
 TGGATGGCATCTGAACAGGGGACTTATTAAGAGCTGATCCTAGTTGAGCCTAGACATGGACATACCTGAAGCTCCTAAACAGAAAACCTGGCGACAAGCGTTGGTGAATCTCATTTGTATGAT 1560
 W M A S E Q G T Y K E L I L V E P S M G H T E A P K A E N W R Q A L V I S L L D 520
 AACAGATCCAGACCTTGCCGTA AAACTCATATGCCGAACCTGACAACACTGATGCTCCACAAGACAGCTCTTTGAAGAAGATTCCACAAGGGTTTTCATGCAATATGCCCTGTTCTC 1680
 N R I Q T L P E K L I C P K L T T L M L Q Q N S S L K K I P T G F F M H M P V L 560
 AGAGTCTTGACTGTGTTACAAGTATCACTGAGATTCCGTGTCTATACAGTATTTGGTGAAGTTGATCATCTGTCTATGTCAGGAACAAGATTAAGTATTTCCACAGAGCTT 1800
 R V L D L S F T S I T E I P L S I K Y L V E L Y H L S M S G T K I S V L P Q E L 600

Fig. 6B

GGGAATCTTAGAAACCTGAGACATCTGACCTACAGAAGACTCTACTTTCTTCAGACGATCCACAGAGATCCATATGTTGGCTGAGCAAGCTCGAGTTCTGAACTTGTACTACAGTTAC 1920
G N L R K L K H L D L Q R T Q F L Q T I P R D A I C W L S K L E V L N L Y Y S Y 640
GCCGGTTGGAACTGCAGAGCTTTGGAGAGATGAGCAGAGAAGAACTCGGATTGCTGACTTGGAATACTGGAATAACCTAACACACACTGGTAATCACTGTCTCTCATTTGGAGACCTTA 2040
A G W E L Q S F G E D E A E E L G E A D L E Y L E N L T T L G I T V L S L E T L 680
AAACCTCTCTTCAGATTCCGTCCTTTCATTAACATATACAGATCTCCAGCTTGAGAGTCGAATGAATCTCCTACTTCATCTCCATCACTCACTCACTAACCATTGCGAGAACTGAGA 2160
K T L F E F G A L H K H I Q H L H V E E C N E L L Y F N L P S L T N H G R N L R 720
AGACTTACCATTAAGCTTGCATGACTTGGAGTAACCTGCTCAGACCCCGAGATTTGAAATGATTGGCTTCCGAGTCTAGAGGTTCTGACGTTACACAGCCTTACAACTTAACAGAGA 2280
R L S I K S C H D L E Y L V T P A D F E N D W L P S L E V L T L H S L H N L T R 760
CTCTGGGGAATTTCTGTAGCCAGATTTCTCGCGAATATCCGTTGCATTAACATTTTCACACTGCACAGACGTAAGAAATGTCCTCATGAGGTTCAAGAACTCCCAAGCTAGAGGTGATT 2400
V W G N S V S Q D C L R N I R C I N I S H C N K L K N V S W V Q K L P K L E V I 800
GAACCTGTTGACTGCAGAGAGATGAGGAATTTGATTAAGCGAACACAGAGAGTCCATCCGTCGAGAGATCCAAATTTGTTCCCAAGCCTGAAGACCTTGAGAACTAGGGATCTGCCAGAACTA 2520
E L F D C R E I E E L I S E H E S P S V E D P T L F P S L K T L R T R D L P E L 840
AACAGATCTCCCATCTCGATTTTCATTCCAAAAAGTTGAACATTAATGATCATCACAAAATGCCCCAGAGTTAAGAAACTGCCGTTTCAGAGAGAGAGACCCAGATGAACCTTGCCAACA 2640
N S I L P S R F S F Q K V E T L V I T N C P R V K K L P F Q E R R T Q M N L P T 880

Fig. 6C

GTTTATTGTGAGGAGAAATGCTGGAACACCTGGAAAAGATCAACCAACGAGAGCTTTGTTATTACCGCGCTTGTCCAAATTGATATAGAGCTAAGACACTGTACAAATA 2760
V Y C E E K W W K A L E K D Q P N E E L C Y L P R F V P N *

TGTCATTCAATAGTACGACGAGAGCCAGAGAGTTGTTCCAGTGAAGTCATCAACTTCCACTAGACCAACAACCTAGACATTATGTAAATCATATAAACCAAACTATCCGGATCAATA 2880

GATTCACGACTATGAGGACGAGACCTCACCGAGTATCGTCCATATGAACCTCAAGCTCCAGTCCGATCAGTGAAGCGAACAAGTTTATCAGATCTCTGCAACAATTCGGGAATC 3000

GTCACCTCAGATTAGACCTCCAGTAAGAAAGTGAAGAAACATGAGACGACGACTGTGAAGATTGAGCTAATGAGCTGAACCGGATCCGGTGAATTGCAGAACCGGATCCGAGAGAAAGAA 3120

TTTTCGATTGTCATCTTATTTTAAATTGTACGTTTGAGCCCAATAATATATGTAGTGAAGCAATAATTCAATGATCAATCAATTTGTAATTTCAAAATTTTCGTAG 3240

TGTAATACGGAAGAAAGAAAGGTCACTGAGT (A)_n

Fig. 6D

consensus PXXaXX LXXLXXLXaXXXX aXXa

505	PKAENW RQALVISLLD NR IQTL	
527	PEKLIC PK LTTLMLQQNSSLKKI	
550	PTGFFMHMPVLRVLDLSFTS ITEI	
574	PLSIKY LVELYHLSMSGTK ISVL	
597	PQELGN LRKLKHLDLQRTQFLQTI	
621	PRDAICWLSKLEVLNLYYSYAGWEL	QSFGEDEAEELG
658	FADLEY LENLTTLGITVLS LETL	KT
683	LFEEGALHKHIQHLHVEECNELLYF	NL
710	P SLTNHGRNLRRLSIKSDHDLEYL	VT
736	PADFENDWLPSLEVLTLSLHNLTRV	WGN
765	SVSQDC LRNIRCINISHCNKLKNV	SWVQKL
795	PK LEV IELFDCREIEELISEHES	PSVED
823	PT LFPSLKTLRTRDLPELNSI L	
845	PSRFS FQKVETLVITNCPRVKKL	

Fig. 7

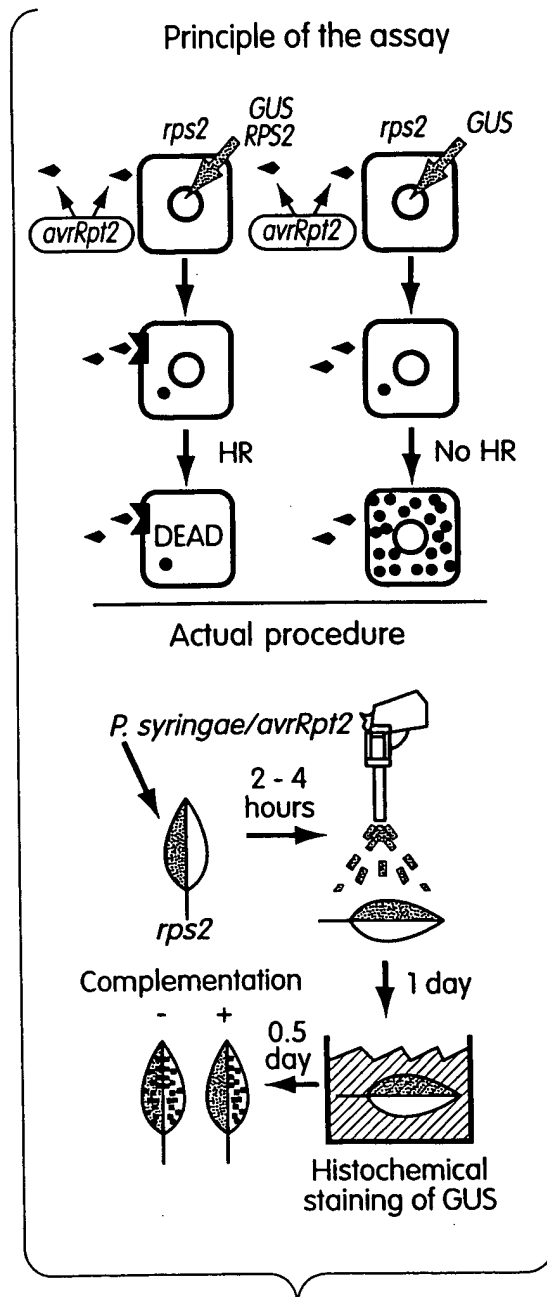


Fig. 9

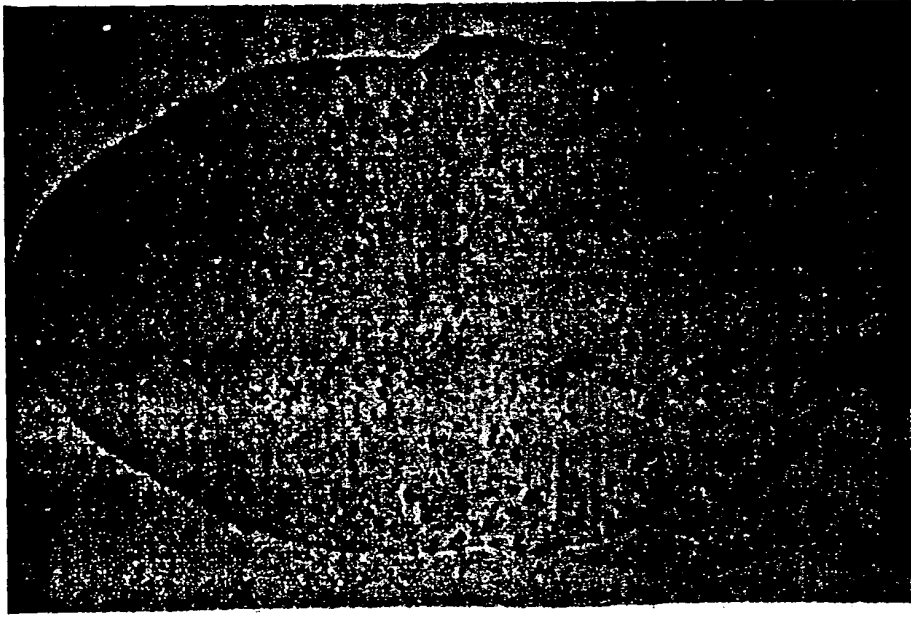


Fig. 10A

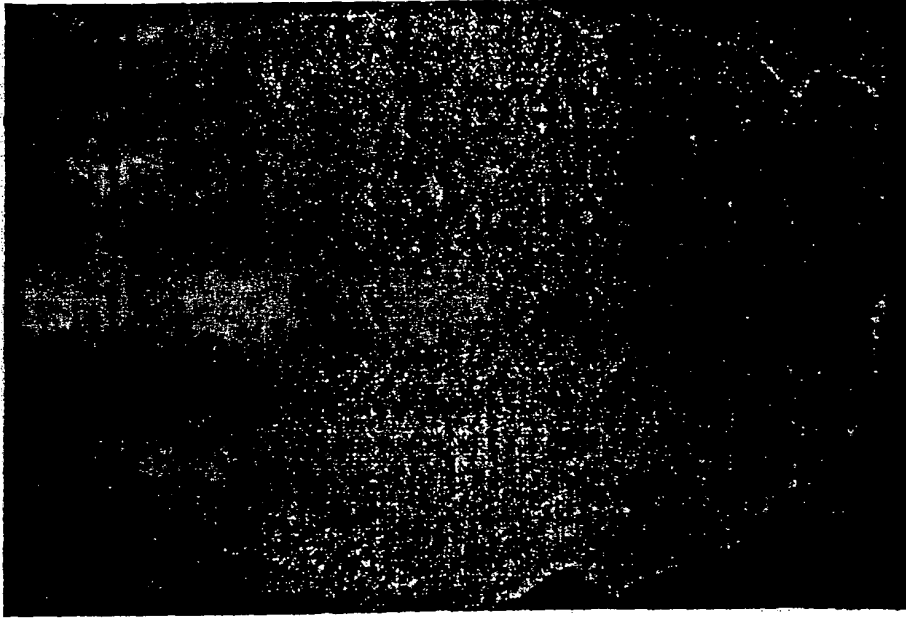


Fig. 10B

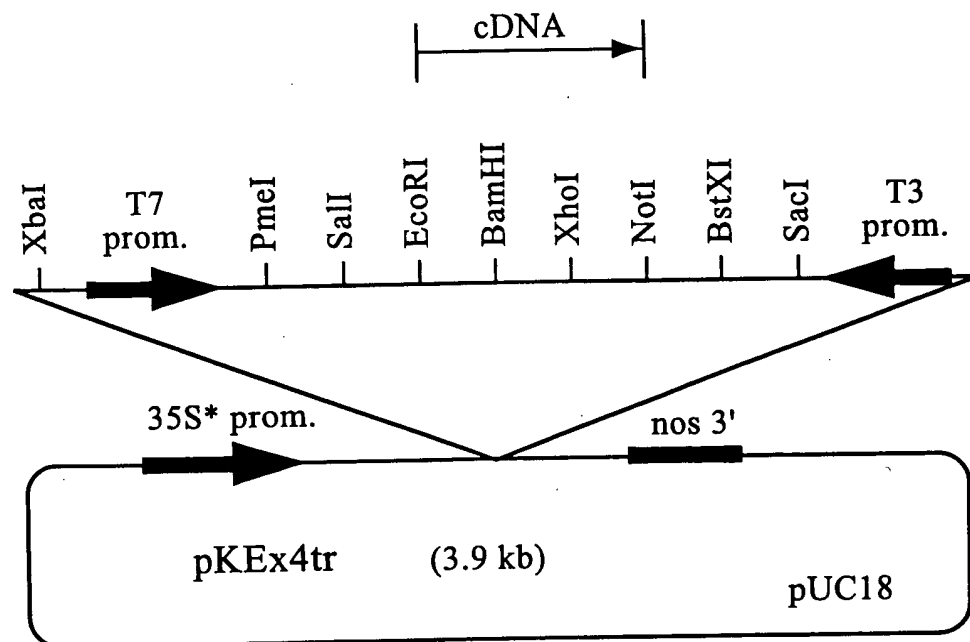


Fig. 11

	10	20	30	40	50	60	
1	aagctttaca	gattggatga	tctcttaatg	catgctgaag	tgactgcaaa	aaggttagca	60
61	atattcagtg	gttctcgta	tgaatatttc	atgaacggaa	gcagcactga	gaaaatgagg	120
121	cccttggtat	ctgattttct	gcaagagatt	gagtctgtca	aggtagagtt	cagaaatggt	180
181	tgcttgcaag	ttctggatat	atcacctttt	tccctgacag	atggagaagg	ccttggtaat	240
241	ttcttattaa	aaaaccaggc	caaggtgccg	aatgatgatg	ctgtttcttc	tgatggaagt	300
301	ttagaggatg	caagcagcac	tgagaaaatg	ggacttccat	ctgattttct	ccgagagatt	360
361	gagtctgttg	agataaagga	ggccagaaaa	ttatatgatc	aagttttgga	tgcaacacat	420
421	tgtgagacga	gtaagcacga	tggaaaaagc	tttatcaaca	ttatgttaac	ccaacaggac	480
481	aaggtgctgg	actatgatgc	tggttcagtg	tcttatcttc	ttaaccaa	ctcagtagtt	540
541	aaagacaaaa	tattgcacat	tggtctttta	cttgtagata	ttgtacagta	ccggaatatg	600
601	catatagaac	ttacagatct	cgctgaacgt	gttcaagata	aaaactacat	tcgtttcttc	660
661	tctgtcaagg	gttatattcc	tgcttggtat	tacacactat	atctctctga	tgtcaagcaa	720
721	ttgcttaagt	ttgttgaggc	agaggtaaag	attatttgtc	tgaaagtacc	agattcttca	780
781	agttatagct	tccctaagac	aaatggatta	ggatatctca	attgcttttt	aggcaaattg	840
841	gaggagcttt	tacgttctaa	gctcgatttg	ataatcgact	taaaacatca	gattgaatca	900
901	gtcaaggagg	gcttattgtg	cctaagatca	ttcattgatc	atttttcaga	aagctatggt	960
961	gagcatgatg	aagcttgtgg	tcttatagca	agagtttctg	taatggcata	caaggctgag	1020
1021	tatgtcattg	actcatgctt	ggcctattct	catccactct	ggtacaaa	tccttggatt	1080
1081	tctgaagttc	ttgagaatat	taagcttgta	aataaagttg	ttggggagac	atgtgaaaga	1140
1141	aggaacactg	aagttactgt	gcatgaagtt	gcaaagacta	ccactaatgt	agcaccatct	1200
1201	ttttcagctt	atactcaaag	agcaaacgaa	gaaatggagg	gttttcagga	tacaatagat	1260
1261	gaattaaagg	ataaactact	tggaggatca	cctgagcttg	atgtcatctc	aatcgttggc	1320
1321	atgccaggat	tgggcaagac	tacactagca	aagaagattt	acaatgatcc	agaagtcacc	1380
1381	tctcgcttcg	atgtccatgc	tcaatgtgtt	gtgactcaat	tatattcatg	gagagagttg	1440
1441	ttgctcacca	ttttgaatga	tgtgcttgag	ccttctgatc	gcaatgaaaa	agaagatgga	1500
1501	gaaatagctg	atgatctacg	ccgatttttg	ttgaccaaga	gattcttgat	tctcattgat	1560
1561	gatgtgtggg	actataaagt	gtgggacaat	ctatgtatgt	gcttcagtga	tgtttcaa	1620
1621	aggagtagaa	ttatccta	aaccgccttg	aatgatgtcg	ccgaatatgt	caaatgtgaa	1680
1681	agtgatcccc	atcatcttcg	tttattcaga	gatgacgaga	gttggacatt	attacagaaa	1740
1741	gaagtctttc	aaggagagag	ctgtccacct	gaacttgaag	atgtgggatt	tgaaatatca	1800
1801	aaaagttgta	gagggttgcc	tctctcagtt	gtgttagtag	ctgggtgtct	gaaacagaaa	1860
1861	aagaagacac	tagattcatg	gaaagtagta	gaacaaagtc	taagttccca	gaggattggc	1920
1921	agcttggaag	agagcata	tataattgga	ttcagttaca	agaatttacc	acactatctt	1980
1981	aagccttggt	ttctctat	tggaggattt	ttgcagggaa	aggatattca	tgactcaaaa	2040
2041	atgaccaagt	tgtgggtagc	tgaagagttt	gtacaagcaa	acaacgaaaa	aggacaagaa	2100
2101	gatacccgca	caaggtttct	tggacgatct	tattggtagg	aatctggtga	tggccatgga	2160
2161	gaagagacct	aatgccaa	tgaaaacgtg	ccgcattcat	gatttgttgc	ataaattctg	2220
2221	catggaaaag	gccaaacaag	aggatttcct	tctccagatc	aataggtaaa	aaaaactgta	2280
2281	ttaattttac	attacaaaaa	aaaagaactg	tattaatttt	actgtattat	gtttatgcc	2340
2341	actctcattt	ccatgtgttc	tcttttat	aattcagtg	agaaggtgta	tttctgaac	2400
2401	gattggaaga	ataccgattg	ttcgttcatt	cttaccaaga	tgaaattgat	ctgtggcgcc	2460
2461	catctcgctc	taatgtccgc	tctttactat	tcaatgcaat	tgatccagat	aacttgttat	2520
2521	ggccgcgtga	tatctccttc	atttttgaga	gcttcaagct	tgtaaagt	ttggatttgg	2580

Fig. 12A

2581 aatcattcaa cattggtggt acctttccca ttgaacaca atatctaatt cagatgaagt 2640
 2641 actttgcggc ccaactgat gaaattcaa ttccttcac tatagctaag ctgaaaaac 2700
 2701 ttgagacttt tgcgtgaaga ggaattggag gagagatgat attacctgt tcaactctga 2760
 2761 agatggatga attgaggcat ataccataa aactcacaat aactaattt ttcttttgt ttgctgcga 2820
 2821 acatggatgt ttaactggt tggtaagac acatttggt tttaaggaa gatgcaaaa ttgagaaaat 2880
 2881 gtctctttta tttaactggt aacttcagg acatttggt tttaaggaa gatgcaaaa ttgagaaaat 2940
 2941 tgagttgcat atttcaggg acatttggt tttaaggaa gatgcaaaa ttgagaaaat 3000
 3001 gttttccag attgatttt ctaagtcacc tttaaggaa gatgcaaaa ttgagaaaat 3060
 3061 atccagccaa acttctcac aagttcaatt tcccttcgca actaaggaa gatgcaaaa ttgagaaaat 3120
 3121 caaagtccg tctactcaga gctttgaag ggaactgca actaaggaa gatgcaaaa ttgagaaaat 3180
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 3241 atgagttt tcttaagt attgactga aacttcagg acctcaga actaaggaa gatgcaaaa ttgagaaaat 3300
 3301 atgagttt tcttaagt attgactga aacttcagg acctcaga actaaggaa gatgcaaaa ttgagaaaat 3360
 3361 atgagttt tcttaagt attgactga aacttcagg acctcaga actaaggaa gatgcaaaa ttgagaaaat 3420
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 3961 atgagttt tcttaagt attgactga aacttcagg acctcaga actaaggaa gatgcaaaa ttgagaaaat 4020
 4021 atgagttt tcttaagt attgactga aacttcagg acctcaga actaaggaa gatgcaaaa ttgagaaaat 4080
 4081 atgagttt tcttaagt attgactga aacttcagg acctcaga actaaggaa gatgcaaaa ttgagaaaat 4140
 4141 atgagttt tcttaagt attgactga aacttcagg acctcaga actaaggaa gatgcaaaa ttgagaaaat 4200
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 5041 atgagttt tcttaagt attgactga aacttcagg acctcaga actaaggaa gatgcaaaa ttgagaaaat 5100
 5101 atgagttt tcttaagt attgactga aacttcagg acctcaga actaaggaa gatgcaaaa ttgagaaaat 5134

Fig. 12B